

1636

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/635,521A

DATE: 04/11/2001
TIME: 09:10:09

Input Set : A:\seqlistcorr.txt
Output Set: N:\CRF3\04112001\I635521A.raw

#6
MZ
4/11/01
ENTERED

3 <110> APPLICANT: Katherine Galvin and Laura A. Rudolph-Owen
5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS
6 AND TREATMENT OF CARDIOVASCULAR AND TUMORIGENIC
7 DISEASE USING 4941
9 <130> FILE REFERENCE: MNI-094
11 <140> CURRENT APPLICATION NUMBER: 09/635,521A
12 <141> CURRENT FILING DATE: 2000-08-09
14 <150> PRIOR APPLICATION NUMBER: 60/199,908
15 <151> PRIOR FILING DATE: 2000-04-26
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: PatentIn Ver. 2.0
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22 <211> LENGTH: 1362
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1359)
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32 Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp
33 1 5 10 15
35 cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc 96
36 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
37 20 25 30
39 ctt att ctg gtg tac ctg atc atc ttc gtg atg gcc ctt ctg ggg aac 144
40 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
41 35 40 45
43 agc gcc acc att cgg gtc acc cag gtg ctg cag aag aaa gga tac ttg 192
44 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
45 50 55 60
47 cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tcg gac atc 240
48 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
49 65 70 75 80
51 ttg gtg ttc ctc atc gcc atg ccc atg gag ttc tac agc atc atc tgg 288
52 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
53 85 90 95
55 aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act 336
56 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
57 100 105 110
59 ttc ctc ttc gag gcc tgc agc tac gct acg ctg ctg cac gtg ctg aca 384
60 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
61 115 120 125
63 ctc agc ttt gag cgc tac atc gcc atc tgt cac ccc ttc agg tac aag 432
64 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
65 130 135 140
67 gct gtg tcg gga cct tgc cag gtg aag ctg ctg att gcc ttc gtc tgg 480

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68 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
69 145                      150                      155                      160
71 gtc acc tcc gcc ctg gtg gca ctg ccc ttg ctg ttt gcc atg ggt act 528
72 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
73                      165                      170                      175
75 gag tac ccc ctg gtg aac gtg ccc agc cac cgg ggt ctc act tgc aac 576
76 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
77                      180                      185                      190
79 cgc tcc agc acc cgc cac cac gag cag ccc gag acc tcc aat atg tcc 624
80 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
81                      195                      200                      205
83 atc tgt acc aac ctc tcc agc cgc tgg acc gtg ttc cag tcc agc atc 672
84 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
85                      210                      215                      220
87 ttc ggc gcc ttc gtg gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc 720
88 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
89 225                      230                      235                      240
91 atg tgc tgg aac atg atg cag gtg ctc atg aaa agc cag aag ggc tcg 768
92 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
93                      245                      250                      255
95 ctg gcc ggg ggc acg cgg cct ccg cag ctg agg aag tcc gag agc gaa 816
96 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
97                      260                      265                      270
99 gag agc agg acc gcc agg agg cag acc atc atc ttc ctg agg ctg att 864
100 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
101                      275                      280                      285
103 gtt gtg aca ttg gcc gta tgc tgg atg ccc aac cag att cgg agg atc 912
104 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
105                      290                      295                      300
107 atg gct gcg gcc aaa ccc aag cac gac tgg acg agg tcc tac ttc cgg 960
108 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
109 305                      310                      315                      320
111 gcg tac atg atc ctc ctc ccc ttc tcg gag acg ttt ttc tac ctc agc 1008
112 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
113                      325                      330                      335
115 tcg gtc atc aac ccg ctc ctg tac acg gtg tcc tcg cag cag ttt cgg 1056
116 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
117                      340                      345                      350
119 cgg gtg ttc gtg cag gtg ctg tgc tgc cgc ctg tcg ctg cag cac gcc 1104
120 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
121                      355                      360                      365
123 aac cac gag aag cgc ctg cgc gta cat gcg cac tcc acc acc gac agc 1152
124 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
125                      370                      375                      380
127 gcc cgc ttt gtg cag cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc 1200
128 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
129 385                      390                      395                      400
131 tct gca agg aga act gag aag att ttc tta agc act ttt cag agc gag 1248
132 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu

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133          405          410          415
135 gcc gag ccc cag tct aag tcc cag tca ttg agt ctc gag tca cta gag 1296
136 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
137          420          425          430
139 ccc aac tca ggc gcg aaa cca gcc aat tct gct gca gag aat ggt ttt 1344
140 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
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144 Gln Glu His Glu Val
145          450
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 453
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
154 Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp
155 1 5 10 15
157 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
158 20 25 30
160 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
161 35 40 45
163 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
164 50 55 60
166 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
167 65 70 75 80
169 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
170 85 90 95
172 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
173 100 105 110
175 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
176 115 120 125
178 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
179 130 135 140
181 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
182 145 150 155 160
184 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
185 165 170 175
187 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
188 180 185 190
190 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
191 195 200 205
193 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
194 210 215 220
196 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
197 225 230 235 240
199 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
200 245 250 255
202 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
203 260 265 270

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205 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
206      275      280      285
208 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
209      290      295      300
211 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
212 305      310      315      320
214 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
215      325      330      335
217 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
218      340      345      350
220 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
221      355      360      365
223 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
224      370      375      380
226 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
227 385      390      395      400
229 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
230      405      410      415
232 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
233      420      425      430
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236      435      440      445
238 Gln Glu His Glu Val
239      450
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 2528
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapiens
247 <220> FEATURE:
248 <221> NAME/KEY: CDS
249 <222> LOCATION: (42)..(1400)
251 <220> FEATURE:
252 <223> OTHER INFORMATION: N at positions 2490 and 2493 may be Adenine,
253      Guanine, Cytosine or Thymine
255 <400> SEQUENCE: 3
256 gggagtcgac ccacgcgtcc ggtagccttg tgctctttct c atg gct tca ccc agc 56
257      Met Ala Ser Pro Ser
258      1      5
260 ctc ccg ggc agt gac tgc tcc caa atc att gat cac agt cat gtc ccc 104
261 Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp His Ser His Val Pro
262      10      15      20
264 gag ttt gag gtg gcc acc tgg atc aaa atc acc ctt att ctg gtg tac 152
265 Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr Leu Ile Leu Val Tyr
266      25      30      35
268 ctg atc atc ttc gtg atg ggc ctt ctg ggg aac agc gcc acc att cgg 200
269 Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn Ser Ala Thr Ile Arg
270      40      45      50
272 gtc acc cag gtg ctg cag aag aaa gga tac ttg cag aag gag gtg aca 248
273 Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu Gln Lys Glu Val Thr

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274      55      60      65
276 gac cac atg gtg agt ttg gct tgc tcg gac atc ttg gtg ttc ctc atc 296
277 Asp His Met Val Ser Leu Ala Cys Ser Asp Ile Leu Val Phe Leu Ile
278 70      75      80      85
280 ggc atg ccc atg gag ttc tac agc atc atc tgg aat ccc ctg acc acg 344
281 Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp Asn Pro Leu Thr Thr
282      90      95      100
284 tcc agc tac acc ctg tcc tgc aag ctg cac act ttc ctc ttc gag gcc 392
285 Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr Phe Leu Phe Glu Ala
286      105      110      115
288 tgc agc tac gct acg ctg ctg cac gtg ctg aca ctc agc ttt gag cgc 440
289 Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr Leu Ser Phe Glu Arg
290      120      125      130
292 tac atc gcc atc tgt cac ccc ttc agg tac aag gct gtg tcg gga cct 488
293 Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys Ala Val Ser Gly Pro
294      135      140      145
296 tgc cag gtg aag ctg ctg att ggc ttc gtc tgg gtc acc tcc gcc ctg 536
297 Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp Val Thr Ser Ala Leu
298 150      155      160      165
300 gtg gca ctg ccc ttg ctg ttt gcc atg ggt act gag tac ccc ctg gtg 584
301 Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val
302      170      175      180
304 aac gtg ccc agc cac cgg ggt ctc act tgc aac cgc tcc agc acc cgc 632
305 Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn Arg Ser Ser Thr Arg
306      185      190      195
308 cac cac gag cag ccc gag acc tcc aat atg tcc atc tgt acc aac ctc 680
309 His His Glu Gln Pro Glu Thr Ser Asn Met Ser Ile Cys Thr Asn Leu
310      200      205      210
312 tcc agc cgc tgg acc gtg ttc cag tcc agc atc ttc ggc gcc ttc gtg 728
313 Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile Phe Gly Ala Phe Val
314      215      220      225
316 gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc atg tgc tgg aac atg 776
317 Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe Met Cys Trp Asn Met
318 230      235      240      245
320 atg cag gtg ctc atg aaa agc cag aag ggc tcg ctg gcc ggg gcc acg 824
321 Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser Leu Ala Gly Gly Thr
322      250      255      260
324 cgg cct ccg cag ctg agg aag tcc gag agc gaa gag agc agg acc gcc 872
325 Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu Glu Ser Arg Thr Ala
326      265      270      275
328 agg agg cag acc atc atc ttc ctg agg ctg att gtt gtg aca ttg gcc 920
329 Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile Val Val Thr Leu Ala
330      280      285      290
332 gta tgc tgg atg ccc aac cag att cgg agg atc atg gct gcg gcc aaa 968
333 Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile Met Ala Ala Ala Lys
334      295      300      305
336 ccc aag cac gac tgg acg agg tcc tac ttc cgg gcg tac atg atc ctc 1016
337 Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg Ala Tyr Met Ile Leu
338 310      315      320      325

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3